

Sequence Listing

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TUMAS, DANIEL B
WOOD, WILLIAM I.

<120> DcR3 Polypeptide, A TNFR Homolog

<130> P1134R2 REVISED

<140> US 09/157,289
<141> 1998-09-18

<150> US 60/059,288
<151> 1997-09-18

<150> US 60/094,640
<151> 1998-07-30

<160> 18

<210> 1
<211> 300
<212> PRT
<213> Homo sapiens

<400> 1
Met Arg Ala Leu Glu Gly Pro Gly Leu Ser Leu Leu Cys Leu Val
1 5 10 15

Leu Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val
20 25 30

Ala Glu Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu
35 40 45

Arg Leu Val Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg
50 55 60

Pro Cys Arg Arg Asp Ser Pro Thr Thr Cys Gly Pro Cys Pro Pro
65 70 75

Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu Arg Cys Arg Tyr
80 85 90

Cys Asn Val Leu Cys Gly Glu Arg Glu Glu Ala Arg Ala Cys
 95 100 105
 His Ala Thr His Asn Arg Ala Cys Arg Cys Arg Thr Gly Phe Phe
 110 115 120
 Ala His Ala Gly Phe Cys Leu Glu His Ala Ser Cys Pro Pro Gly
 125 130 135
 Ala Gly Val Ile Ala Pro Gly Thr Pro Ser Gln Asn Thr Gln Cys
 140 145 150
 Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala Ser Ser Ser Ser Ser
 155 160 165
 Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala Leu Gly Leu Ala
 170 175 180
 Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu Cys Thr Ser
 185 190 195
 Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala Glu Glu
 200 205 210
 Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile Ser
 215 220 225
 Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu
 230 235 240
 Gly Trp Gly Pro Thr Pro Arg Ala Gly Arg Ala Ala Leu Gln Leu
 245 250 255
 Lys Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly
 260 265 270
 Ala Leu Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met
 275 280 285
 Pro Gly Leu Glu Arg Ser Val Arg Glu Arg Phe Leu Pro Val His
 290 295 300

<210> 2
 <211> 1114
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> Unsure
 <222> 1090

<223> Unknown base

<400> 2

tccgcaggcg gaccgggggc aaaggagggtg gcatgtcggt caggcacagc 50
agggtcctgt gtccgcgctg agccgcgctc tccctgctcc agcaaggacc 100
atgagggcgc tggagggggcc aggcctgtcg ctgctgtgcc tgggtttggc 150
gctgcctgcc ctgctgcgg tgccggctgt acgcggagtg gcagaaaacac 200
ccacacctcc ctggcgggac gcagagacag gggagcggct ggtgtgcgcc 250
cagtcccccc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300
cacgacgtgt ggcccggtgc caccgcgcca ctacacgcag ttctggaact 350
acctggagcg ctgcgcgtac tgcaacgtcc tctgcgggaa gcgtgaggag 400
gaggcacggg cttgccacgc cacccacaac cgtgcctgcc gctgccgcac 450
cggcttcttc ggcacgcgtg gtttctgctt ggagcacgca tcgtgtccac 500
ctggtgccgg cgtgattgcc ccgggcaccc ccagccagaa cacgcagtgc 550
cagccgtgcc ccccaggcac cttctcagcc agcagctcca gctcagagca 600
gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc 650
caggctcttc ctcccatgac accctgtgca ccagctgcac tggcttcccc 700
ctcagcacca gggtaccagg agctgaggag tgtgagcgtg ccgtcatcga 750
ctttgtggct ttccaggaca tctccatcaa gaggctgcag cggctgctgc 800
aggccctcga ggccccggag ggctggggtc cgacaccaag ggccggccgc 850
gcggccttgc agctgaagct gcgtcgccgg ctcacggagc tcctggggc 900
gcaggacggg ggcgtgctgg tgccggctgt gcagggcgctg cgcgtggcca 950
ggatgcccg gctggagcgg agcgtccgtg agcgcttctt ccctgtgcac 1000
tgatcctggc cccctcttat ttattctaca tccttggcac cccacttgca 1050
ctgaaagagg cttttttta aatagaagaa atgaggttn taaaaaaaaa 1100
aaaaaaaaaa aaaa 1114

<210> 3

<211> 491

Q
E
G
G
G
G
E
E
E
E
T
D
A

<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 62, 73, 86, 98
<223> unknown base

<400> 3
ggcgagacag ccccacgacg tgtggcccg gtccaccgcg ccactacacg 50
cagttctgga antaactgga gcnctgccgc tactgnaacg tcctctgngg 100
ggagcgtgag gaggaggcac gggcttgcca cgccacccac aaccgtgcct 150
ggcgctgccg caccggcttc ttgcgcacg ctggttctg cttggagcac 200
gcacatcggtgc cacctgggtgc cggcgtgatt gccccgggca ccccccagcca 250
gaacacgcac tgccttagccg tgccccccag gcacccctctc agccagcagc 300
tccagctcaag agcagtgccca gccccaccgc aactgcacgg ccctgggcct 350
ggccctcaat gtgccaggct cttccctccca tgacaccctg tgcaccagct 400
gcactggctt ccccccctcagc accagggtac caggagctga ggagtgtgag 450
cgtgccgtca tcgactttgt ggcttccag gacatctcca t 491

<210> 4
<211> 73
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 4
ggcgagacag ccccacgacg tgtggcccg gtccaccgcg ccactacacg 50
cattctggaa ctacctggag cgc 73

<210> 5
<211> 271
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233

<223> unknown base

<400> 5

gccgagacag cccccacgacg tgtggcccggt gtccaccgcg cnactacacg 50

cagttctgga antaactgga gcncgtccgc tactgnaacg tcctctgngg 100

ggagcntgag gaggaggcan gngcttgcca cgccacccac aaccgcgcct 150

gcngctgcag caccggnttc ttgcgcacg ctgnnttctg cttggagcac 200

gcatcgtgtc cacctggtn cggcgtgatt gcncgggca cccccagcca 250

gaacacgcat gcaaagccgt g 271

<210> 6

<211> 201

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 182

<223> unknown base

<400> 6

gcagttctgg aactacctgg agcgctgccg ctactgcaac gtcctctgct 50

gggagcgtga ggaggaggca cgggcttgcc acgccaccca caaccgtgcc 100

tgcgcgtgcc gcaccggctt ctgcgcac gctggttct gcttggagca 150

cgcacatcgtgt ccacctggtg ccggcgtgat tncccccgggc acccccagcc 200

a 201

<210> 7

<211> 277

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

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<220>
<221> unsure
<222> 142
<223> unknown base

<400> 7
gagggggcccc caggagtggt ggccggaggt gtggcagggg tcaggttgct 50
ggtcccagcc ttgcaccctg agctaggaca ccagttcccc tgaccctgtt 100
cttccctcct ggctgcaggc acccccagcc agaacacgca gnccagccgt 150
cccccccccagg cacttctca gccagcagct ccagtcaga gcagtgccag 200
ccccaccgca actgcacggc cctgggcctg gccctcaatg tgccaggctc 250
ttcctccat gacaccctgt gcaccag 277

<210> 8
<211> 199
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 8
gcatcgtgtc cacctgggtgc cggcgtgatt gccccgggca ccccccagcca 50
gaacacgcag gcctagccgt gccccccagg cacttctca gccagcagct 100
ccagtcaga gcagtgccag ccccaccgca actgcacggc cctgggcctg 150
gccctcaatg tgccaggctc ttcctccat gacaccctgt gcaccagct 199

<210> 9
<211> 226
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 4, 9, 12, 165
<223> unknown base

<400> 9
agcngtgcnc cncaggcacc ttctcagcca gcagttccag ctcagagcag 50

tgccagcccc accgcaactg cacggccctg ggcctggccc tcaatgtgcc 100
aggctttcc tcccatgaca cgctgtgcac cagctgcact ggcttcccc 150
tcagcaccag ggtancagga gctgaggagt gtgagcgtgc cgtcatcgac 200
tttggcctt tccaggacat ctccat 226

<210> 10
<211> 283
<212> DNA
<213> Homo sapiens

<220>
<221> Unsure
<222> 1-283
<223> Unknown organism

<220>
<221> unsure
<222> 27, 64, 140
<223> unknown base

<400> 10
tttgtccacc tggtgccggc gtgattnccc gggcacccccc agccagaaca 50
cgcaagtgcga gccntcccccc caggcacctt ctcagccagc agctccagct 100
cagagcagtgc ccagccccac cgcaactgca acgcccgtgn ctggccctca 150
atgtgccagg ctcttcctcc catgacacccc tgtgcaccag ctgcactggc 200
ttccccctca gcaccagggt accaggagct gaggagtgtg agcgtgccgt 250
catcgactttt gtggcttcc aggacatctc cat 283

<210> 11
<211> 21
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 11
cacgctggtt tctgcttggaa g 21

<210> 12
<211> 22
<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 12
agctggtgca cagggtgtca tg 22

<210> 13
<211> 53
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<400> 13
cccaggcacc ttctcagcca gccagcagct ccagtcaga gcagtgccag 50
ccc 53

<210> 14
<211> 24
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<400> 14
acacgatgcg tgctccaagc agaa 24

<210> 15
<211> 17
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<400> 15
cttcttcgcg cacgctg 17

<210> 16
<211> 16
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<400> 16
atcacgccgg caccag 16

<210> 17
<211> 461
<212> PRT
<213> Homo sapiens

<400> 17
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu
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Leu Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr
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Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr
35 40 45
Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly
50 55 60
Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
65 70 75
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val
80 85 90
Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val
95 100 105
Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
110 115 120
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg
125 130 135
Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
140 145 150
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala
155 160 165
Pro Gly Thr Phe Ser Asn Thr Ser Ser Thr Asp Ile Cys Arg
170 175 180
Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser
185 190 195
Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala
200 205 210

Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln
215 220 225

His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr
245 250 255

Gly Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala
260 265 270

Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr
275 280 285

Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val
290 295 300

Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu
305 310 315

Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser Ser
320 325 330

Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg
335 340 345

Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu
350 355 360

Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His
365 370 375

Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser
380 385 390

Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met
395 400 405

Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln
410 415 420

Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu
425 430 435

Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro
440 445 450

Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
455 460

<210> 18
<211> 293
<212> PRT
<213> Homo sapiens

<400> 18
Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
1 5 10 15
Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
20 25 30
Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
35 40 45
Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
50 55 60
Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Asp Ser Trp His
65 70 75
Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
80 85 90
Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
95 100 105
Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
110 115 120
His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
125 130 135
Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
140 145 150
Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
155 160 165
Cys Ser Val Phe Gly Leu Leu Thr Gln Lys Gly Asn Ala Thr
170 175 180
His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
185 190 195
Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala
200 205 210
Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp
215 220 225

Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
245 250 255

Leu Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile
260 265 270

Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
275 280 285

Gly His Ala Asn Leu Thr Phe Glu
290

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